



SEQUENCE LISTING

<110> Junghans, Richard P.

<120> Antibodies as Chimeric Effector Cell Receptors Against Tumor Antigens

<130> 003

<140> 10/066,773

<141> 2001-10-12

<150> 60/250,089

<151> 2000-11-30

<160> 19

<170> PatentIn version 3.1

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<212> DNA

<213> Homo sapiens and Mus sp.

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<221> CDS

<222> (2428)..(3759)

<223> Chimeric IgTCR sequence contained in retroviral vector. Retroviral vector sequence (non-coding regions) are incidental to the invention. The translated (coding region) is relevant to the invention. (pertinent to Figure 3.)

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Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr	
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Cys Lys Ala Ser Gln Asp Val Gly Thr Ser Val Ala Trp Tyr Gln Gln	
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Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Trp Thr Ser Thr Arg	
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His Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp	
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Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr	
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caa cct ggc cgg tcc ctg cgc ctg tcc tgc tcc gca tct ggc ttc gat Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Phe Asp	155	160	165 2934
ttc acc aca tat tgg atg agt tgg gtg aga cag gca cct gga aaa ggt Phe Thr Thr Tyr Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly	170	175	180 2982
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acg cca gcg ccg cga cca cca aca ccg gcg ccc acc atc gcg tcg cag Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln	270	275	280 3270
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Gln Gly Gln Asn Gln Leu	Tyr Asn Glu Leu Asn	Leu Gly Arg Arg Glu	
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Glu Tyr Asp Val Leu Asp	Lys Arg Arg Gly Arg	Asp Pro Glu Met Gly	
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Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val  
 35 40 45

Gly Thr Ser Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys  
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# Antibodies as Chimeric Effector Cells ST25

Leu Leu Ile Tyr Trp Thr Ser Thr Arg His Thr Gly Val Pro Ser Arg  
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Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser  
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Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Leu  
100 105 110

Tyr Arg Ser Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Gly Gly  
115 120 125

Ser Gly Ser Gly Gly Ser Gly Ser Gly Gly Ser Gly Ser Glu Val Gln  
130 135 140

Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg  
145 150 155 160

Leu Ser Cys Ser Ala Ser Gly Phe Asp Phe Thr Thr Tyr Trp Met Ser  
165 170 175

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile Gly Glu Ile  
180 185 190

His Pro Asp Ser Ser Thr Ile Asn Tyr Ala Pro Ser Leu Lys Asp Arg  
195 200 205

Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Phe Leu Gln Met  
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Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys Ala Ser Leu  
225 230 235 240

Tyr Phe Gly Phe Pro Trp Phe Ala Tyr Trp Gly Gln Gly Thr Pro Val  
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Thr Val Ser Ser Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro Pro  
260 265 270

Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu  
275 280 285

Ala Ala Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp  
290 295 300

Phe Ala Leu Asp Pro Lys Leu Cys Tyr Leu Leu Asp Gly Ile Leu Phe  
305 310 315 320

Ile Tyr Gly Val Ile Leu Thr Ala Leu Phe Leu Arg Val Lys Phe Ser  
325 330 335

Arg Ser Ala Glu Pro Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr  
340 345 350

Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys  
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Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn  
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Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu  
385 390 395 400

Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly  
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Gly Val Gln Cys Glu Val Val Val Val Glu Ser Gly Gly Gly Phe Val	
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Lys Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ala Gly Phe Thr	
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ttc agt aga tat gcc atg tct tgg gtt cgc cag act ccg gag aag agg	194
Phe Ser Arg Tyr Ala Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg	
50 55 60	
ctg gag tgg gtc gca acc ata agt agt ggt ggt agt cac acc tac tat	242
Leu Glu Trp Val Ala Thr Ile Ser Ser Gly Gly Ser His Thr Tyr Tyr	
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Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys	
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Asn Thr Leu Tyr Leu Gln Met Ser Ser Leu Arg Ser Glu Asp Thr Ala	
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ata tat tac tgt gca aga ccg ggt tac gac agg ggg gcc tgg ttt ttc	386
Ile Tyr Tyr Cys Ala Arg Pro Gly Tyr Asp Arg Gly Ala Trp Phe Phe	
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Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser	
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Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ala Gly Phe Thr Phe  
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Ser Arg Tyr Ala Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu  
50 55 60

Glu Trp Val Ala Thr Ile Ser Ser Gly Gly Ser His Thr Tyr Tyr Pro  
65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn  
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Thr Leu Tyr Leu Gln Met Ser Ser Leu Arg Ser Glu Asp Thr Ala Ile  
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Val Thr Pro Gly Asp Ser Val Ser Leu Ser Cys Arg Ala Ser Gln Ile  
 35 40 45

Ile Ser Asn Asn Leu His Trp Tyr Gln Gln Lys Ser His Glu Ser Pro  
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Arg Leu Leu Ile Lys Tyr Ala Ser Gln Ser Ile Ser Gly Ile Pro Ser  
 65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn  
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<222> (1)..(258)
<223> Light chain leader plus sFv of MB3.6
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<400> 7                    nnnnnnnnnnnn                    60

gatatcagat ctcagctgtc tagacatatg gttttcacac ctcagatann nnnnnnnnnnnn 30  
nnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnngggac aaagctggag 120

atcaaagggtg gctcaggatc ggggtggagcc ggctctgggtg gctcaggatc ggaagtgggtg 180

gtggtggagn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnacc 240

acggtcaccg tctccagt 258

<210> 8

<211> 682

<212> DNA

<213> Mus sp.

 $\langle 220 \rangle$ 

<221> CDS

<222> (20) .. (418)

```
<222> (20)..(418)
<223> 3D8 Heavy chain V region, plus leader
```

<400> 8  
 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32  
 ... tta att tta att gtc 52

tgaacacgga cccctcacc atg aac ttc ggg ctc agc ttg att ttc ctt gtc  
Met Asn Phe Gly Leu Ser Leu Ile Phe Leu Val  
1 5 10

ctt gtt tta aaa ggt gtc cag tgt gaa gtg aag gtg gtg gag tct ggg 100  
 Leu Val Leu Lys Gly Val Gln Cys Glu Val Lys Val Val Glu Ser Gly  
 15 20 25

gga ggc tta gtg aag cct gga gcg tct ctg aaa ctc tcc tgt gca gcc 148  
Gly Gly Leu Val Lys Pro Gly Ala Ser Leu Lys Leu Ser Cys Ala Ala  
30 35 40

tct gga ttc act ttc agt aac tat ggc atg tct tgg gtt cgc cag act 196  
Ser Gly Phe Thr Phe Ser Asn Tyr Gly Met Ser Trp Val Arg Gln Thr  
45 50 55

tca gac aag agg ctg gag tgg gtc gca tcc att agt agt ggt ggt gat 244  
Ser Asp Lys Arg Leu Glu Trp Val Ala Ser Ile Ser Ser Gly Gly Asp  
60 65 70 75

agc acc ttc tat gca gac aat gta aag ggc cga ttc acc atc tcc aga 292  
 Ser Thr Phe Tyr Ala Asp Asn Val Lys Gly Arg Phe Thr Ile Ser Arg  
 80 85 90

gag aat gcc aag aac acc ctg tac ctg caa atg agt agt ctg aag tct 340  
 Glu Asn Ala Lys Asn Thr Leu Tyr Leu Gln Met Ser Ser Leu Lys Ser  
 95 100 105

gag gac acg gcc ttg tat tac tgt gca aga gac gat cta ttt aac tgg 388  
 Glu Asp Thr Ala Leu Tyr Tyr Cys Ala Arg Asp Asp Leu Phe Asn Trp  
 110 115 120

ggc caa ggc acc act ctc aca gtc tca tca gccaaaacaa cagccccatc 438  
 Gly Gln Gly Thr Thr Leu Thr Val Ser Ser  
 125 130

ggtctatcca ctggcccctg tgtgtggaga tacaattggc tcctcgggtga ctttaggatg 498

cctggtcaag gggtatttcc ttgagccagt gaccttgacc tggaactctg gatccctgtc 558

cagtgggtgtg cacatcttcc cagctgtctt gcagtctgac ctctacaccc tcagcagctc 618

agtgactgta acctcgagca cctggcccag ccagtccatc acttgcaatg tggcccaccc 678

ggca 682

<210> 9  
 <211> 133  
 <212> PRT  
 <213> Mus sp.

<400> 9

Met Asn Phe Gly Leu Ser Leu Ile Phe Leu Val Leu Val Leu Lys Gly  
 1 5 10 15

Val Gln Cys Glu Val Lys Val Val Glu Ser Gly Gly Gly Leu Val Lys  
 20 25 30

Pro Gly Ala Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe  
 35 40 45

Ser Asn Tyr Gly Met Ser Trp Val Arg Gln Thr Ser Asp Lys Arg Leu



50

55

60

Glu Trp Val Ala Ser Ile Ser Ser Gly Gly Asp Ser Thr Phe Tyr Ala  
65 70 75 80

Asp Asn Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala Lys Asn  
85 90 95

Thr Leu Tyr Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Leu  
100 105 110

Tyr Tyr Cys Ala Arg Asp Asp Leu Phe Asn Trp Gly Gln Gly Thr Thr  
115 120 125

Leu Thr Val Ser Ser  
130

<210> 10  
<211> 729  
<212> DNA  
<213> Mus sp.

<220>  
<221> CDS  
<222> (15)..(410)  
<223> 3D8 Light chain V region, plus leader

<400> 10  
ccgttgccgt cgtg atg agt cct gcc cag ttc ctg ttt ctg tta gtg ctc 50  
Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu  
1 5 10  
tgg att cag gaa acc aac ggt gat gtt gta atg acc cag act cca ctc 98  
Trp Ile Gln Glu Thr Asn Gly Asp Val Val Met Thr Gln Thr Pro Leu  
15 20 25  
act ttg tcg gtt acc att gga caa cca gcc tct atc tct tgc aag tca 146  
Thr Leu Ser Val Thr Ile Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser  
30 35 40  
agt cag agc ctc tta tat agt aat gga aaa acc tat ttg aat tgg tta 194

Ser	Gln	Ser	Leu	Leu	Tyr	Ser	Asn	Gly	Lys	Thr	Tyr	Leu	Asn	Trp	Leu		
45					50					55					60		
tta	cag	agg	cca	ggc	cag	tct	cca	aag	cgc	cta	atc	tat	ctg	gtg	tct		242
Leu	Gln	Arg	Pro	Gly	Gln	Ser	Pro	Lys	Arg	Leu	Ile	Tyr	Leu	Val	Ser		
				65					70					75			
aaa	ctg	gac	tct	gga	gtc	cct	gac	agg	ttc	act	ggc	agt	gga	tca	gga		290
Lys	Leu	Asp	Ser	Gly	Val	Pro	Asp	Arg	Phe	Thr	Gly	Ser	Gly	Ser	Gly		
			80					85					90				
aca	gat	ttt	aca	ctg	aaa	atc	agc	aga	gtg	gag	gct	gag	gat	ttg	gga		338
Thr	Asp	Phe	Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Leu	Gly		
		95					100					105					
gtt	tat	tac	tgc	gtg	caa	ggc	aca	cat	ttt	cct	cac	acg	ttc	gga	ggg		386
Val	Tyr	Tyr	Cys	Val	Gln	Gly	Thr	His	Phe	Pro	His	Thr	Phe	Gly	Gly		
	110					115				120							
ggg	acc	aag	ctg	gaa	ata	aaa	cgg	gctgatgctg	caccaactgt	atccatcttc							440
Gly	Thr	Lys	Leu	Glu	Ile	Lys	Arg										
125					130												
ccaccatcca	gtgagcagtt	aacatctgga	ggtgcctcag	tcgtgtgctt	cttgaacaac												500
ttctacccca	aagacatcaa	tgtcaagtgg	aagattgatg	gcagtgaacg	acaaaatggc												560
gtcctgaaca	gttggactga	tcaggacagc	aaagacagca	cctacagcat	gagcagcacc												620
ctcacgttga	ccaaggacga	gtatgaacga	cataacagct	atacctgtga	ggccactcac												680
aagacatcaa	cttcacccat	tgtcaagagc	ttcaacagga	atgagtgtt													729

<210> 11  
 <211> 132  
 <212> PRT  
 <213> Mus sp.

<400> 11

Met	Ser	Pro	Ala	Gln	Phe	Leu	Phe	Leu	Leu	Val	Leu	Trp	Ile	Gln	Glu	
1				5					10					15		

Thr	Asn	Gly	Asp	Val	Val	Met	Thr	Gln	Thr	Pro	Leu	Thr	Leu	Ser	Val	
		20						25					30			

Thr Ile Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu  
35 40 45

Leu Tyr Ser Asn Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg Pro  
50 55 60

Gly Gln Ser Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser  
65 70 75 80

Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr  
85 90 95

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys  
100 105 110

Val Gln Gly Thr His Phe Pro His Thr Phe Gly Gly Gly Thr Lys Leu  
115 120 125

Glu Ile Lys Arg  
130

<210> 12  
<211> 736  
<212> DNA  
<213> Mus sp.

<220>  
<221> CDS  
<222> (14)..(430)  
<223> 4D4 Heavy chain V region, plus leader

<400> 12  
actgactcta acc atg gga tgg aga tgg atc ttt ctt ttc ctc ctg tca 49  
Met Gly Trp Arg Trp Ile Phe Leu Phe Leu Leu Ser  
1 5 10

gga act gca ggt gtc cat tgc cag gtt cag ctg cag cag tct gga cct 97  
Gly Thr Ala Gly Val His Cys Gln Val Gln Leu Gln Gln Ser Gly Pro  
15 20 25

gag ctg gtg aag cct ggg gct tta gtg aag ata tcc tgc aag gct tct	145
Glu Leu Val Lys Pro Gly Ala Leu Val Lys Ile Ser Cys Lys Ala Ser	
30 35 40	
ggt tac acc ttc aca agc tac gat ata aac tgg gtg aag cag agg cct	193
Gly Tyr Thr Phe Thr Ser Tyr Asp Ile Asn Trp Val Lys Gln Arg Pro	
45 50 55 60	
gga cag gga ctt gag tgg att gga tgg att tat cct gga gat ggt ggt	241
Gly Gln Gly Leu Glu Trp Ile Gly Trp Ile Tyr Pro Gly Asp Gly Gly	
65 70 75	
act aat tac aat gag aaa ttc aag ggc aag gcc aca ctg act gca gac	289
Thr Asn Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp	
80 85 90	
aaa tcc tcc agc aca gcc tac atg cag ctc agt agc ctg act tct gag	337
Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu	
95 100 105	
aac tct gca gtc tat ttc tgt gca aga ggg ggt aac ttc cct tct tat	385
Asn Ser Ala Val Tyr Phe Cys Ala Arg Gly Gly Asn Phe Pro Ser Tyr	
110 115 120	
gct atg gac tac tgg ggt caa gga acc tca gtc acc gtc tcc tca	430
Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser	
125 130 135	
gccaaaacga cccccccatc tgtctatcca ctggcccctg gatctgctgc ccaaactaac	490
tccatgggtga ccccgggatg cctgggtcaag ggctatttcc ctgagccagt gacagtgacc	550
tggaactctg gatccctgtc cagcgggtgtg cacaccttcc cagctgtcct gcagtctgac	610
ctctacactc tgagcagctc agtgactgtc cctccagca cctggcccag cgagaccgtc	670
acctgcaacg ttgccacccc ggccagcagc accaagggtgg acaagaaaat tgtgcccagg	730
gattgt	736

<210> 13  
 <211> 139  
 <212> PRT  
 <213> Mus sp.

<400> 13

Met Gly Trp Arg Trp Ile Phe Leu Phe Leu Leu Ser Gly Thr Ala Gly  
 1 5 10 15

Val His Cys Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys  
 20 25 30

Pro Gly Ala Leu Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
 35 40 45

Thr Ser Tyr Asp Ile Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu  
 50 55 60

Glu Trp Ile Gly Trp Ile Tyr Pro Gly Asp Gly Gly Thr Asn Tyr Asn  
 65 70 75 80

Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser  
 85 90 95

Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asn Ser Ala Val  
 100 105 110

Tyr Phe Cys Ala Arg Gly Gly Asn Phe Pro Ser Tyr Ala Met Asp Tyr  
 115 120 125

Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser  
 130 135

<210> 14  
 <211> 504  
 <212> DNA  
 <213> Mus sp.

<220>  
 <221> CDS  
 <222> (7)..(402)  
 <223> 4D4 Light chain V region, plus leader

<400> 14  
ctcaaa atg aag ttg cct gtt agg ctg ttg gtg ctg atg ttc tgg att 48  
Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile  
1 5 10

cct gct tcc aac agt gat gtt ttg atg acc caa tct cca ctc tcc ctg 96  
Pro Ala Ser Asn Ser Asp Val Leu Met Thr Gln Ser Pro Leu Ser Leu  
15 20 25 30

cct gtc agt ctt gga gat caa gcc tcc atc tct tgc aga tct agt cag 144  
Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln  
35 40 45

agc att gtc cat agt aat gga gac acc tat tta gaa tgg tac ctg cag 192  
Ser Ile Val His Ser Asn Gly Asp Thr Tyr Leu Glu Trp Tyr Leu Gln  
50 55 60

aaa cca ggc cag tct cca aag ctg ctg atc tac aag gtt tcc gac cga 240  
Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asp Arg  
65 70 75

ttt tct ggg gtc cca gac agg ttc agt ggc agt gga tca ggg aca gat 288  
Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp  
80 85 90

ttc aca ctc aag atc agc aga gtg gag gct gag gat ctg gga gtt tat 336  
Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr  
95 100 105 110

ttc tgc ttt caa ggt tca cat gtt ccg tac gcg ttc gga ggg ggg acc 384  
Phe Cys Phe Gln Gly Ser His Val Pro Tyr Ala Phe Gly Gly Gly Thr  
115 120 125

aag ctg gaa ata aaa cgg gctgatgctg caccaactgt atccatcttc 432  
Lys Leu Glu Ile Lys Arg  
130

ccaccatcca gtgagcagtt aacatctgga ggtgcctcag tcgtgtgctt cttgaacaac 492

ttctacccca aa 504

<210> 15  
<211> 132  
<212> PRT  
<213> Mus sp.

<400> 15

Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro Ala  
 1 5 10 15

Ser Asn Ser Asp Val Leu Met Thr Gln Ser Pro Leu Ser Leu Pro Val  
 20 25 30

Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile  
 35 40 45

Val His Ser Asn Gly Asp Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro  
 50 55 60

Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asp Arg Phe Ser  
 65 70 75 80

Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr  
 85 90 95

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys  
 100 105 110

Phe Gln Gly Ser His Val Pro Tyr Ala Phe Gly Gly Gly Thr Lys Leu  
 115 120 125

Glu Ile Lys Arg  
 130

<210> 16  
 <211> 761  
 <212> DNA  
 <213> Mus sp.

<220>  
 <221> CDS  
 <222> (62)..(478)  
 <223> 3E11 Heavy chain V region, plus leader

<400> 16  
cctggattca atttccagtt cctcacattc agtgatcagc actgaacacg gacccctcac 60  
c atg aac ttc ggg ctc agc ttg att ttc ctt gtc ctt gtt tta aaa ggt 109  
Met Asn Phe Gly Leu Ser Leu Ile Phe Leu Val Leu Val Leu Lys Gly  
1 5 10 15  
gtc cag tgt gaa gtg aaa ctg gtg gag tct ggg gga gac tta atg aac 157  
Val Gln Cys Glu Val Lys Leu Val Glu Ser Gly Gly Asp Leu Met Asn  
20 25 30  
cct gga gcg tct ctg aaa ctc tcc tgt gca gcc tct gga ttc agt ttc 205  
Pro Gly Ala Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe  
35 40 45  
agt aac tat ggc atg tct tgg gtt cgc cag act tca gac aag agg ctg 253  
Ser Asn Tyr Gly Met Ser Trp Val Arg Gln Thr Ser Asp Lys Arg Leu  
50 55 60  
gag tgg gtc gct tcc att agt acg ggt ggt gct aat acc ttc tat cca 301  
Glu Trp Val Ala Ser Ile Ser Thr Gly Gly Ala Asn Thr Phe Tyr Pro  
65 70 75 80  
gac aat gta aag ggc cga ttc acc att tcc aga gag aat gcc aag aac 349  
Asp Asn Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala Lys Asn  
85 90 95  
acc cta tac ctg caa atg agt agt ctg aag tct gag gac acg gcc ttg 397  
Thr Leu Tyr Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Leu  
100 105 110  
tat ttc tgt gca aga gat agt cac tcc gta ggt tgt tgg ttt gct acc 445  
Tyr Phe Cys Ala Arg Asp Ser His Ser Val Gly Cys Trp Phe Ala Thr  
115 120 125  
tgg ggc caa ggg act ctg gtc act gtc tct gca gccaaaacaa ccccccatc 498  
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala  
130 135  
agtctatcca ctggcccctg ggtgtggaga tactactggt tcctccgtga ctctgggatg 558  
cctgggtcaag ggctacttcc ctgagtcagt gactgtgact tggaactccg gatccctgcc 618  
cagcagtgtg cacaccttcc cagctctcct gcagtctgga ctctacacta tgagcagctc 678  
agtgactgtc ccctccagca cctggccaag ccagaccgtt acctgcagtg ttgctcaccc 738  
agccagcagc accacgggtgg aca 761



<210> 17  
 <211> 139  
 <212> PRT  
 <213> Mus sp.

<400> 17

Met Asn Phe Gly Leu Ser Leu Ile Phe Leu Val Leu Val Leu Lys Gly  
 1 5 10 15

Val Gln Cys Glu Val Lys Leu Val Glu Ser Gly Gly Asp Leu Met Asn  
 20 25 30

Pro Gly Ala Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe  
 35 40 45

Ser Asn Tyr Gly Met Ser Trp Val Arg Gln Thr Ser Asp Lys Arg Leu  
 50 55 60

Glu Trp Val Ala Ser Ile Ser Thr Gly Gly Ala Asn Thr Phe Tyr Pro  
 65 70 75 80

Asp Asn Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala Lys Asn  
 85 90 95

Thr Leu Tyr Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Leu  
 100 105 110

Tyr Phe Cys Ala Arg Asp Ser His Ser Val Gly Cys Trp Phe Ala Thr  
 115 120 125

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala  
 130 135

<210> 18  
 <211> 698  
 <212> DNA



gttggactga tcaggacagc aaagacagca cctacagcat gagcagcacc ctcacgttga 621  
ccaaggacga gtatgaacga cataacagct atacctgtga ggccactcac aagacatcaa 681  
cttcacccat cgtcaag 698

<210> 19  
<211> 132  
<212> PRT  
<213> Mus sp.

<400> 19

Met Gly Ile Lys Met Glu Ser Gln Thr Leu Val Phe Ile Ser Ile Leu  
1 5 10 15

Leu Trp Leu Tyr Gly Ala Asp Gly Asn Ile Val Met Thr Gln Ser Pro  
20 25 30

Lys Ser Met Ser Met Ser Val Gly Glu Arg Val Thr Leu Thr Cys Lys  
35 40 45

Ala Ser Glu Asn Val Val Thr Tyr Val Ser Trp Tyr Gln Gln Lys Pro  
50 55 60

Glu Gln Ser Pro Lys Leu Leu Ile Tyr Gly Ala Ser Asn Arg Tyr Thr  
65 70 75 80

Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Ala Thr Asp Phe Thr  
85 90 95

Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Asp Tyr His Cys  
100 105 110

Gly Gln Gly Tyr Ser Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu  
115 120 125

Glu Ile Lys Arg

Ant dies as Chimeric Effector Cell. ST25

130